SEQUENCE LISTING

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Avissar, P.
Walker, K.
Metz, R.

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        35                  40                  45
Lys Ser Gly Thr Met Leu Asn Gly Ser Val Ile Arg Pro Val Lys Val
    50                  55                  60
Thr Ala Ser Val Ser Thr Ser Glu Lys Ala Ser Glu Ile Val Leu Gln
65                  70                  75                  80
Pro Ile Arg Glu Ile Ser Gly Leu Ile Lys Leu Pro Gly Ser Lys Ser
                85                  90                  95
Leu Ser Asn Arg Ile Leu Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr
            100                 105                 110
Val Val Asp Asn Leu Leu Asn Ser Asp Asp Ile Asn Tyr Met Leu Asp
        115                 120                 125
Ala Leu Lys Lys Leu Gly Leu Asn Val Glu Arg Asp Ser Val Asn Asn
    130                 135                 140
Arg Ala Val Val Glu Gly Cys Gly Gly Ile Phe Pro Ala Ser Leu Asp
145                 150                 155                 160
Ser Lys Ser Asp Ile Glu Leu Tyr Leu Gly Asn Ala Gly Thr Ala Met
                165                 170                 175
Arg Pro Leu Thr Ala Ala Val Thr Ala Ala Gly Gly Asn Ala Ser Tyr
            180                 185                 190
Val Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro Ile Gly Asp Leu
        195                 200                 205
Val Val Gly Leu Lys Gln Leu Gly Ala Asp Val Glu Cys Thr Leu Gly
    210                 215                 220
Thr Asn Cys Pro Pro Val Arg Val Asn Ala Asn Gly Gly Leu Pro Gly
225                 230                 235                 240
Gly Lys Val Lys Leu Ser Gly Ser Ile Ser Ser Gln Tyr Leu Thr Ala
                245                 250                 255
Leu Leu Met Ala Ala Pro Leu Ala Leu Gly Asp Val Glu Ile Glu Ile
            260                 265                 270
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Phe Phe Val Lys Gly Gly Gln Lys Tyr Lys Ser Pro Gly Asn Ala Tyr
305 310 315 320
Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Gly Ala Ala
325 330 335
Ile Thr Gly Glu Thr Val Thr Val Glu Gly Cys Gly Thr Thr Ser Leu
340 345 350
Gln Gly Asp Val Lys Phe Ala Glu Val Leu Glu Lys Met Gly Cys Lys
355 360 365
Val Ser Trp Thr Glu Asn Ser Val Thr Val Thr Gly Pro Ser Arg Asp
370 375 380
Ala Phe Gly Met Arg His Leu Arg Ala Val Asp Val Asn Met Asn Lys
385 390 395 400
Met Pro Asp Val Ala Met Thr Leu Ala Val Val Ala Leu Phe Ala Asp
405 410 415
Gly Pro Thr Thr Ile Arg Asp Val Ala Ser Trp Arg Val Lys Glu Thr
420 425 430
Glu Arg Met Ile Ala Ile Cys Thr Glu Leu Arg Lys Leu Gly Ala Thr
435 440 445
Val Glu Glu Gly Ser Asp Tyr Cys Val Ile Thr Pro Pro Ala Lys Val
450 455 460
Lys Pro Ala Glu Ile Asp Thr Tyr Asp Asp His Arg Met Ala Met Ala
465 470 475 480
Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Val Thr Ile Lys Asp Pro
485 490 495
Gly Cys Thr Arg Lys Thr Phe Pro Asp Tyr Phe Gln Val Leu Glu Ser
500 505 510
Ile Thr Lys His
515

<210> 27
<211> 516
<212> PRT
<213> Petunia hybrida

<400> 27
Met Ala Gln Ile Asn Asn Met Ala Gln Gly Ile Gln Thr Leu Asn Pro
1 5 10 15
Asn Ser Asn Phe His Lys Pro Gln Val Pro Lys Ser Ser Ser Phe Leu
20 25 30
Val Phe Gly Ser Lys Lys Leu Lys Asn Ser Ala Asn Ser Met Leu Val
35 40 45
Leu Lys Lys Asp Ser Ile Phe Met Gln Lys Phe Cys Ser Phe Arg Ile
50 55 60
Ser Ala Ser Val Ala Thr Ala Gln Lys Pro Ser Glu Ile Val Leu Gln
65 70 75 80
Pro Ile Lys Glu Ile Ser Gly Thr Val Lys Leu Pro Gly Ser Lys Ser
85 90 95
Leu Ser Asn Arg Ile Leu Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr
100 105 110
Val Val Asp Asn Leu Leu Ser Ser Asp Asp Ile His Tyr Met Leu Gly
115 120 125
Ala Leu Lys Thr Leu Gly Leu His Val Glu Glu Asp Ser Ala Asn Gln
130 135 140
Arg Ala Val Val Glu Gly Cys Gly Gly Leu Phe Pro Val Gln Lys Glu

Arg Pro Leu Thr Ala Ala Val Thr Val Ala Gly Gly Asn Ser Arg Tyr
180 185 190
Val Leu Asp Gly Val Pro Arg Met Arg Glu Arg Pro Ile Ser Asp Leu
195 200 205
Val Asp Gly Leu Lys Gln Leu Gly Ala Glu Val Asp Cys Phe Leu Gly
210 215 220
Thr Lys Cys Pro Pro Val Arg Ile Val Ser Lys Gly Gly Leu Pro Gly
225 230 235 240
Gly Lys Val Lys Leu Ser Gly Ser Ile Ser Ser Gln Tyr Leu Thr Ala
245 250 255
Leu Leu Met Ala Ala Pro Leu Ala Leu Gly Asp Val Glu Ile Glu Ile
260 265 270
Ile Asp Lys Leu Ile Ser Val Pro Tyr Val Glu Met Thr Leu Lys Leu
275 280 285
Met Glu Arg Phe Gly Ile Ser Val Glu His Ser Ser Ser Trp Asp Arg
290 295 300
Phe Phe Val Arg Gly Gly Gln Lys Tyr Lys Ser Pro Gly Lys Ala Phe
305 310 315 320
Val Glu Gly Asp Ala Ser Ser Ala Ser Tyr Phe Leu Ala Gly Ala Ala
325 330 335
Val Thr Gly Gly Thr Ile Thr Val Glu Gly Cys Gly Thr Asn Ser Leu
340 345 350
Gln Gly Asp Val Lys Phe Ala Glu Val Leu Glu Lys Met Gly Ala Glu
355 360 365
Val Thr Trp Thr Glu Asn Ser Val Thr Val Lys Gly Pro Pro Arg Ser
370 375 380
Ser Ser Gly Arg Lys His Leu Arg Ala Ile Asp Val Asn Met Asn Lys
385 390 395 400
Met Pro Asp Val Ala Met Thr Leu Ala Val Val Ala Leu Tyr Ala Asp
405 410 415
Gly Pro Thr Ala Ile Arg Asp Val Ala Ser Trp Arg Val Lys Glu Thr
420 425 430
Glu Arg Met Ile Ala Ile Cys Thr Glu Leu Arg Lys Leu Gly Ala Thr
435 440 445
Val Glu Glu Gly Pro Asp Tyr Cys Ile Ile Thr Pro Pro Glu Lys Leu
450 455 460
Asn Val Thr Asp Ile Asp Thr Tyr Asp Asp His Arg Met Ala Met Ala
465 470 475 480
Phe Ser Leu Ala Ala Cys Ala Asp Val Pro Val Thr Ile Asn Asp Pro
485 490 495
Gly Cys Thr Arg Lys Thr Phe Pro Asn Tyr Phe Asp Val Leu Gln Gln
500 505 510
Tyr Ser Lys His
515

<210> 28
<211> 444
<212> PRT
<213> Zea mays

<400> 28
Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly
1 5 10 15
Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu

Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
50 55 60
Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
65 70 75 80
Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe
85 90 95
Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110
Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
115 120 125
Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140
Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
145 150 155 160
Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser
165 170 175
Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala
180 185 190
Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
195 200 205
Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
210 215 220
Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
225 230 235 240
Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
245 250 255
Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
260 265 270
Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
275 280 285
Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
290 295 300
Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
305 310 315 320
Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
325 330 335
Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
340 345 350
Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
355 360 365
Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys
370 375 380
Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
385 390 395 400
Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
405 410 415
Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
420 425 430
Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
435 440

<210> 29
<211> 64
<212> DNA

<400> 29
cgtttccacc tgcagcagtg accgcagcgg taagtggacg cattgctgtt gctgcattac 60
cgag 64

<210> 30
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant primer

<400> 30
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cgag 64

<210> 31
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant primer

<400> 31
cgtttccacc tgcagcagtg accgcagcgg taagtgaacg cattgctatt cctgcattac 60
cgag 64

<210> 32
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant primer

<400> 32
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cgag 64

<210> 33
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant primer

<400> 33
cgtttccacc tgcagcagtg accgcagcgg taagtgaacg cattgctatt gctgcattac 60
cgag 64

<210> 34
<211> 64

<223> Mutant primer

<400> 34
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cgag 64

<210> 35
<211> 64
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<213> Artificial Sequence

<220>
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<400> 35
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cgag 64

<210> 36
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant primer

<400> 36
cgtttccacc tgcagcagtg accgcagcgg taagtgaacg cattgctaat cctgcattac 60
cgag 64

<210> 37
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
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<400> 37
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cgag 64

<210> 38
<211> 64
<212> DNA
<213> Artificial Sequence

<220>
<223> Mutant primer

<400> 38
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cgag 64

<400> 39
Leu Phe Leu Gly Asn
1 5

<210> 40
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 40
gctctagaga aagcgtcgga gattgtactt 30

<210> 41
<211> 41
<212> DNA
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<220>
<223> Primer

<400> 41
gcagatctga gctcttagtg ctttgtgatt ctttcaagta c 41

<210> 42
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 42
gcgtctagaa aaacgagata aggtgcag 28

<210> 43
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 43
gcggatcctc aggatttttt cgaaagctta tttaaatg 38

<210> 44
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<212> DNA
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